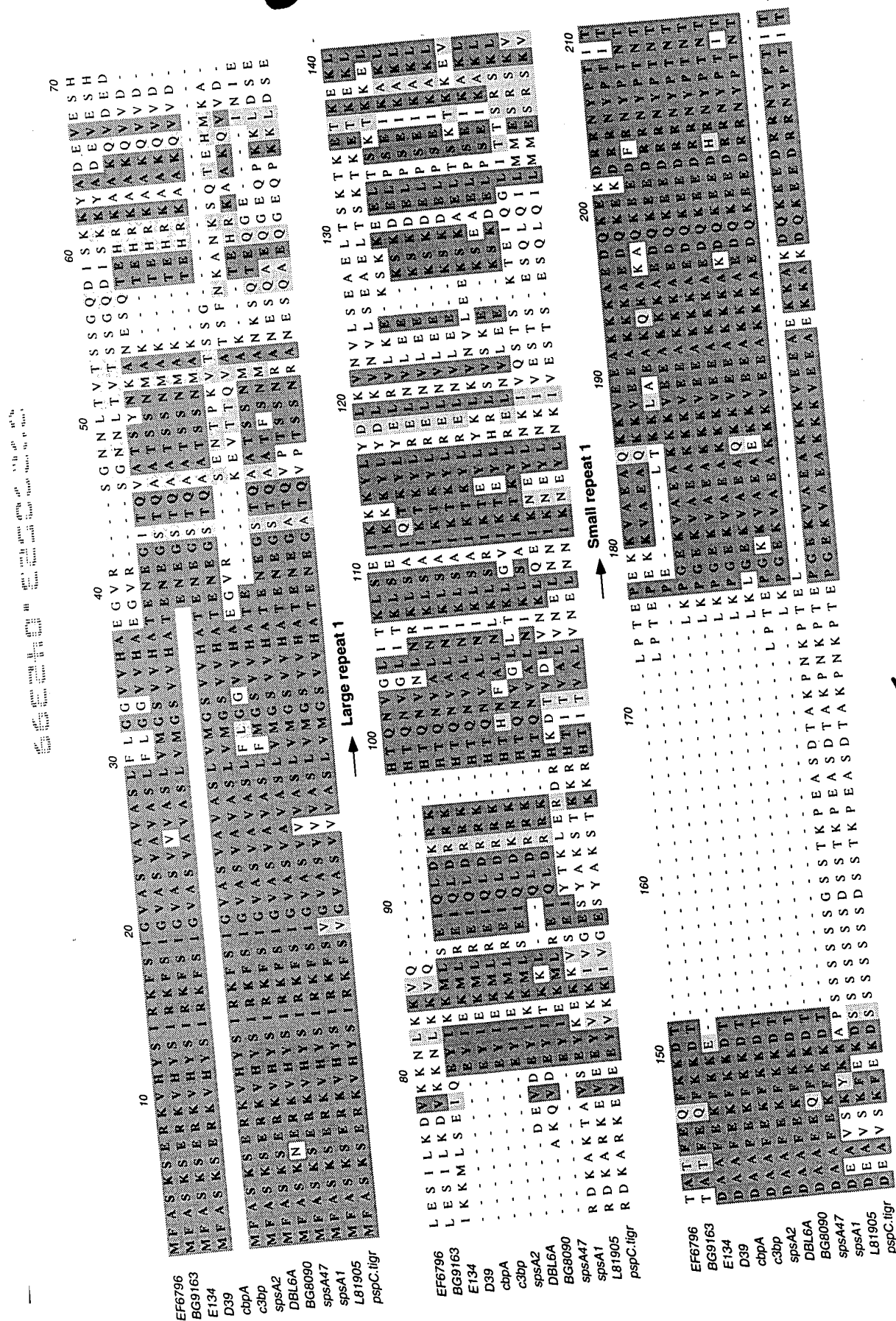


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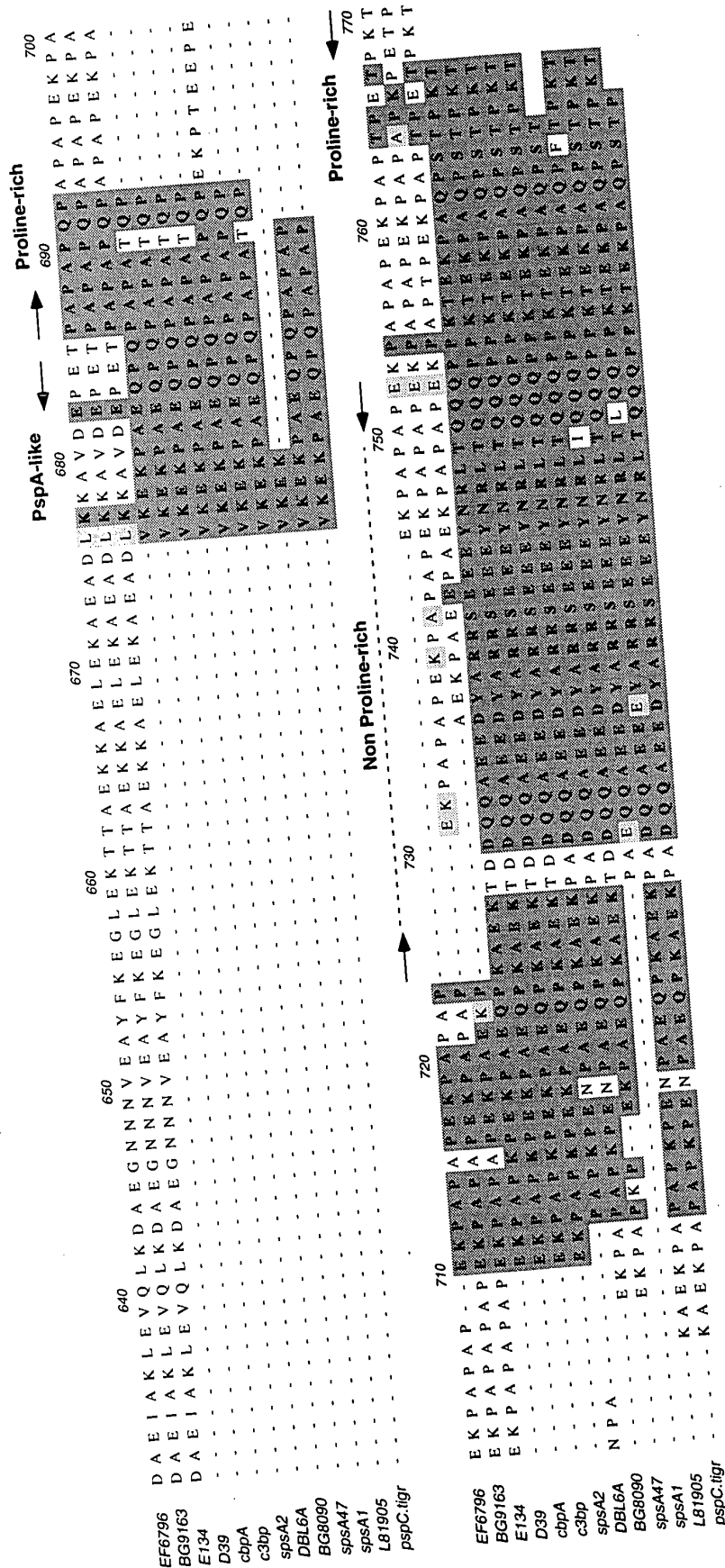


Fig. 2 (cont'd)

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	a	b	c	d	e	f	g	
1								Glu Gly Val Arg Ser Gly Asn Asn Leu Thr
11								Val Thr Ser Ser Gly
16		Gln	Asp	Ile	Ser	Lys	Lys	
22	Tyr	Ala	Asp	Glu	Val	Glu	Ser	
29		His	Leu	Glu	Ser	Ile		
34	Leu	Lys	Asp	Val	Lys	Lys	Asn	
41	Leu	Lys	Lys					
44	Val	Gln	His	Thr	Gln	Asn	Val	
51		Gly	Leu	Ile	Thr	Lys		
56	Leu	Ser	Glu	Ile	Lys	Lys	Lys	
63							Tyr	
64	Leu	Tyr	Asp	Leu	Lys			
69	Val	Asn	Val	Leu	Ser	Glu	Ala	
76		Glu	Leu	Thr	Ser	Lys		
81			Thr	Lys	Glu	Thr		
85	Lys	Glu	Lys	Leu	Thr	Ala	Thr	
92	Phe	Glu	Gln	Phe	Lys	Lys	Asp	
99								Thr Leu Pro Thr Glu Pro
105				Glu	Lys	Lys		
108	Val	Ala	Glu	Ala	Gln	Lys	Lys	
115	Val	Glu	Glu	Ala	Lys	Lys	Lys	
122			Ala	Glu	Asp	Gln		
126	Lys	Glu	Lys	Asp	Arg	Arg	Asn	
133	Tyr	Pro	Thr	Ile	Thr			
138	Tyr	Lys	Thr	Leu	Glu	Leu	Glu	
145	Ile	Ala	Glu	Ser	Asp	Val	Glu	
152	Val	Lys	Lys	Ala	Glu	Leu	Glu	
159	Leu	Val	Lys	Val	Lys	Ala	Lys	
166	Glu	Ser	Gln	Asp	Glu	Glu	Lys	
173	Ile	Lys	Gln	Ala	Glu	Ala	Glu	
180	Val	Glu	Ser	Lys	Gln	Ala	Glu	
187			Ala	Thr	Arg			
190	Leu	Lys	Lys	Ile	Lys	Thr	Asp	
197	Arg	Glu	Glu	Ala	Lys	Arg	Lys	
204		Ala	Asp	Ala	Lys	Leu	Lys	
210		Glu	Ala	Val	Glu	Lys	Asn	
216	Val	Ala	Thr	Ser	Glu	Gln	Asp	
223	Lys							
224								Pro Lys Arg Arg Ala Lys Arg Gly Val Ser
234								Gly Glu Leu Ala Thr Pro Asp Lys Lys Glu
244								Asn Asp Ala Lys Ser Ser Asp Ser Ser Val
254								Gly Glu Glu Thr Leu Pro Ser Pro Ser Leu
264								Asn Met Ala Asn
268				Glu	Ser	Gln		
271		Thr	Glu	His	Arg	Lys	Asp	
277	Val	Asp	Glu	Tyr				
281	Ile	Lys	Lys	Met	Leu	Ser	Glu	
288	Ile	Gln	Leu	Asp	Arg	Arg	Lys	
295		His	Thr	Gln	Asn	Val		
300		Asn	Leu	Asn	Ile	Lys		
305	Leu	Ser	Ala	Ile	Lys	Thr	Lys	
312			Tyr	Leu	Tyr	Glu		
316	Leu	Ser	Val	Leu	Lys	Glu	Asn	
323				Ser	Lys			
325	Lys	Glu	Glu	Leu	Thr	Ser	Lys	
332			Thr	Lys	Ala	Glu		
336	Leu	Thr	Ala	Ala	Phe	Glu	Gln	

FIG. 3

page 1

343	Phe Lys Lys	
346		Asp Thr Leu Lys Pro
351		Glu Lys Lys
354	Val Ala Glu Ala Glu Lys Lys	
361	Val Glu Glu Ala Lys Lys Lys	
368		Ala Lys Asp Gln
372	Lys Glu Glu Asp Arg Arg Asn	
379		Tyr
380		Pro Thr Asn Thr
384	Tyr Lys Thr Leu Glu Leu Glu	
391	Ile Ala Glu Ser Asp Val Lys	
398	Val Lys Glu Ala Glu	
403	Leu Glu Leu Val Lys Glu Glu	
410	Ala Asn Glu Ser Arg Asn Glu	
417		Glu Lys Ile Lys Gln Ala
423	Lys Glu Lys Val Glu Ser Lys	
430	Lys Ala Glu Ala Thr Arg	
436	Leu Glu Lys Ile Lys Thr Asp	
443	Arg Lys Lys Ala Glu Glu Glu	
450		Ala Lys Arg Lys
454	Ala Glu Glu Ser Glu Lys Lys	
461	Ala Ala Glu Ala Lys Gln Lys	
468	Val Asp Ala Glu Glu Tyr Ala	
475		Leu Glu Ala Lys
479	Ile Ala Glu Leu Glu Tyr Glu	
486	Val Gln Arg Leu Glu Lys Glu	
493	Leu Lys Glu	
496	Ile Asp Glu Ser Asp Ser Glu	
503		Asp Tyr Leu Lys Glu Gly
509	Leu Arg Ala	
512		Pro Leu Gln Ser Lys
517	Leu Asp Thr Lys Lys Ala Lys	
524	Leu Ser Lys	
527	Leu Glu Glu Leu Ser Asp Lys	
534	Ile Asp Glu Leu Asp Ala Glu	
541	Ile Ala Lys Leu Glu Val Gln	
548	Leu Lys Asp Ala Glu Gly Asn	
555		Asn Asn
557	Val Glu Ala Tyr Phe Lys Glu	
564		Gly Leu Glu Lys Thr
569		Thr Ala Glu Lys Lys
574		Ala Glu Leu Glu Lys Ala
580	Glu Ala Asp Leu Lys Lys Ala	
587	Val Asp Glu	

**Figure 3.** The coiled-coil motif of the  $\alpha$ -helix of PspC. Amino acids that are not in the coiled-coil motif are in the right column. This is the output from the Matcher program accessed through the Internet (<http://catt.poly.edu/~jps/>).

*Fig. 3 (cont'd)*

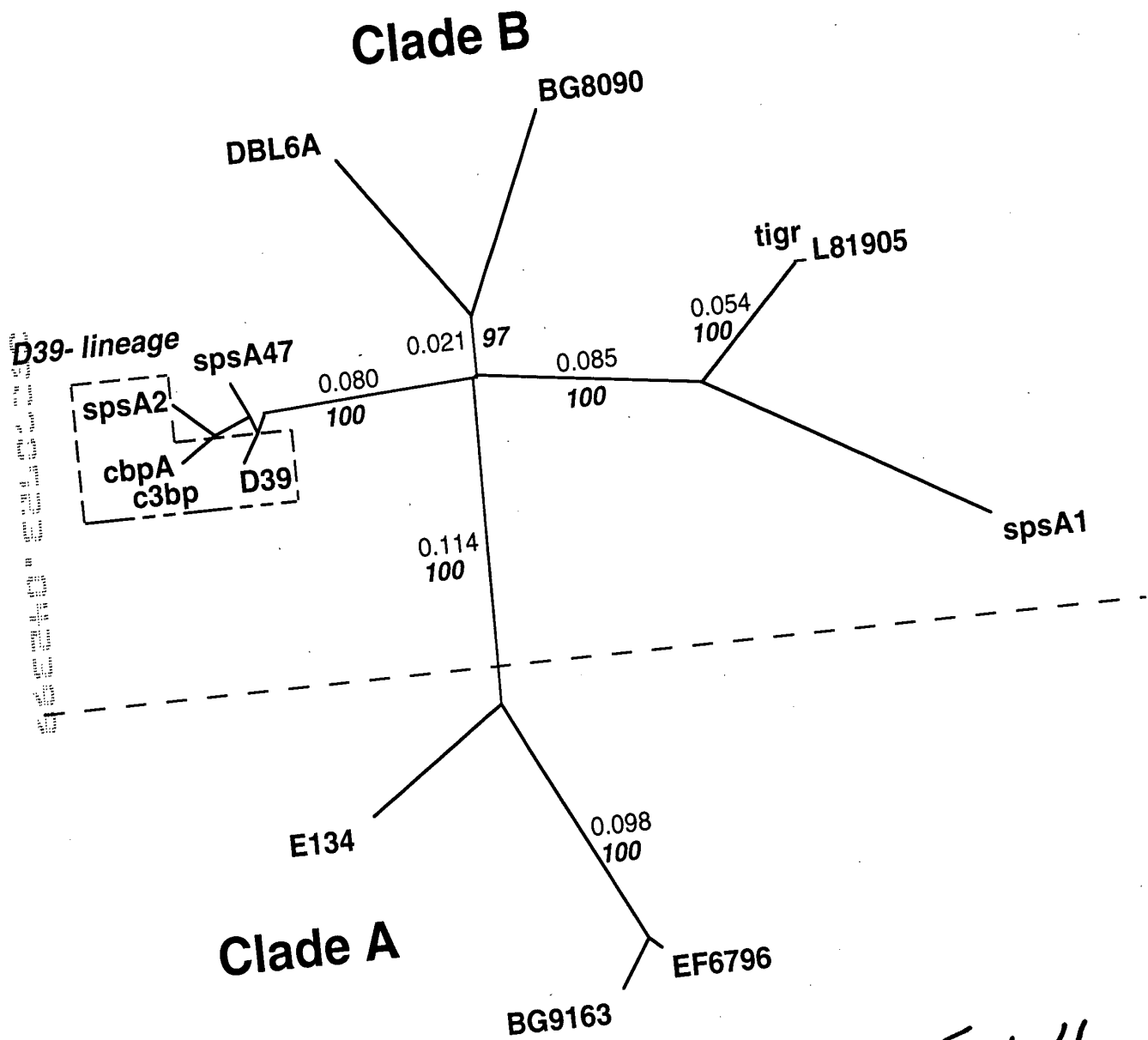


Fig. 4



FIGURE 5. Choline-binding Domain

PspC consensus

11111111112  
12345678901234567890

- 1 KTGWKQENGWYFYNTDGSMA
- 2 TGWLQNNGSWYYLNAMGAMA
- 3 TGWLQNNGSWYYLNANGSMA
- 4 TGWLQNNGSWYYLNANGAMA
- 5 TGWLQYNGSWYYLNANGDMA
- 6 TGWLQYNGSWYYLNSNGAMA
- 7 TGWLQYNGSWYYLNANGDMA
- 8 TGWLQNNGSWYYLNANGDMA
- 9 TGWLQYN SWYYLNANGDMA
- 10 TGWVKDGDWYYLEASGAMKA
- 11 SQWFKVSDKWYYVNGSGALA

VNTTVDGYGVNANGWVN

18 amino acid tail PspC  
28% identical to consensus

TGWLQNNGSWYYLNANGAMA PspC consensus repeat

Y

For PspA/R36A alignment see Yother and Briles 1992.

TGWLQXNGSWYYLNANGAMA

Y

PspA/Rx1 consensus

95% identical to PspC consensus

VNTTVDGYKVNANGEWV\_

PspA/Rx1 17 amino acid tail.  
One AA different from PspC,  
And one AA shorter.

Fig. 5

PspA/EF5668

11111111112

12345678901234567890

1 IGWKQENGMWYFYNTDGSM A  
2 TGWLQNNGSWYYLNSNGAM A  
3 TGWLQYNGSWYYLNANGAM A  
4 TGWLQYNGSWYYLNANGAM A  
5 TGWLQYNGSWYYLNANGDM A  
6 TGWLQYNGSWYYLNANGDM A  
7 TGWAKVHGSWYYLNANGSM A  
8 TGWVKDGETWYYLEASGSMKA  
9 NQWFQVSDKWYYVNGLGSL S  
10 VNTTVDGYKVNANGEWV

17 amino acid tail EF5668 PspA

TGWLQYNGSWYYLNANGSM A

PspA/EF5668 consensus

90% identical to PspC consensus

#### Repeat #1

PspC consensus

KTGWKQENGNWYFYNTDGSM A

PspA/Rx1

TGWKQENGMWYFYNTDGSM A

PspA/EF5668

IGWKQENGMWYFYNTDGSM A

#### Repeat #N-1

PspC consensus

TGWVKDGDWYYLEASGAMKA

PspA/Rx1

TGWVKDGDWYYLEASGAMKA

PspA/EF5668

TGWVKDGETWYYLEASGSMKA

#### Repeat #N

PspC consensus

SQWFKVSDKWYYVNGSGALA

PspA/Rx1

SQWFKVSDKWYYVNGLGALA

PspA/EF5668

NQWFQVSDKWYYVNGLGSL S

#### 17-18 AA tail

PspC consensus

VNTTVDGYGVNANGEWVN

PspA/Rx1

VNTTVDGYKVNANGEWV

PspA/EF5668

VNTTVDGYKVNANGEWV

Fig. 5 (cont'd)

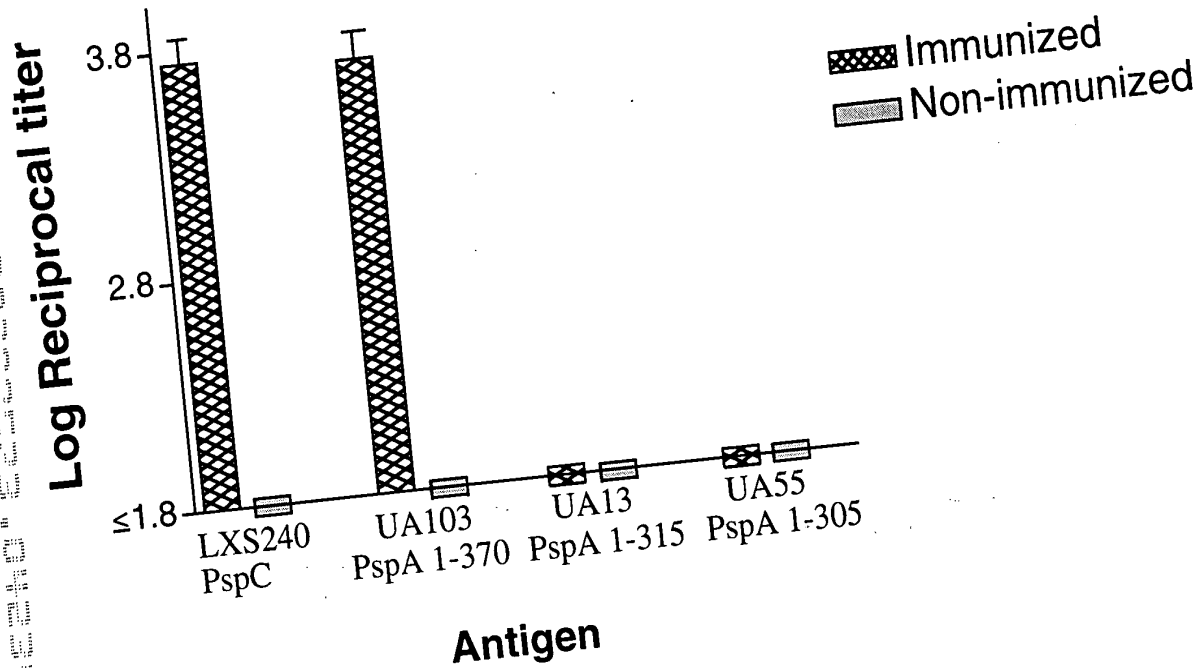
**A**

Strain	Anti-PspC Polyclonal	Anti-PspA Monoclonal
JY53	+	+
D39	+	+
WU2	+	-
JY1119	+	+
L81905	+	+
EF6796	+	+
BG7322	+	+
BG9163	+	+
A66	+	+

**Figure 6.** Western Immunoblot of pneumococcal lyates. Panel A was developed with anti-PspC polyclonal serum and panel B was developed with anti-PspA monoclonal antibody, Xi126. The molecular weight markers are indicated. Cross-reaction of the polyclonal serum to PspC is observed with all strains tested.

Fig. 6

# Log Reciprocal titer of serum from PspC-immunized mice



**Figure 7.** Level of antibody reactive to PspC and PspA fragments present in the sera of mice immunized with PspC. Each bar represents the mean of the log reciprocal titer and upperbound of standard error of sera from five mice. The limit of detection of the log reciprocal antibody titer is 1.8.

FIG. 7

Fig. 8

Other Formats:

Links:

LOCUS CAA05158 539 aa BCT 14-OCT-1997  
 DEFINITION SpsA protein.  
 ACCESSION CAA05158  
 PID g2576331  
 VERSION CAA05158.1 GI:2576331  
 DBSOURCE embl locus SPSPSA2, accession AJ002054.1  
 KEYWORDS  
 SOURCE Streptococcus pneumoniae.  
 ORGANISM Streptococcus pneumoniae  
 Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
 Streptococcus.  
 REFERENCE 1 (residues 1 to 539)  
 AUTHORS Hammerschmidt,S.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-OCT-1997) Hammerschmidt S., Microbiology, Division  
 Microbial Pathogenesis, National Research Centre for Biotechnology,  
 Spielmannstrasse 7, 38106 Braunschweig, GERMANY  
 REFERENCE 2 (residues 1 to 539)  
 AUTHORS Hammerschmidt,S., Talay,S.R., Brandtzaeg,P. and Chhatwal,G.S.  
 TITLE SpsA, a novel pneumococcal surface protein with specific binding to  
 secretory immunoglobulin A and secretory component  
 JOURNAL Mol. Microbiol. 25 (6), 1113-1124 (1997)  
 MEDLINE 98010350  
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 121 akldaafekf kkdtklpgke vaeakkkvee akkkaedqke edrnpyntnt yktleleiae  
 181 fdvkvkael elvkeeakef megtikqak ekveskkaea trleniktdr kkaeeeaark  
 241 aaeedkvkek paeqpqpapa tqepkppkp ekpaeqpkae ktddqqaeed yarrseeeyn  
 301 rltqqppkt ekpaqpstpk tgwkqengmw yfyntdgsma tgwlqnnsw yylnangama  
 361 tgwlqnnsw yylnangama tgwlqnnsw yylnangama tgwlqyngsw yylnsngama

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the above report in format

Other Formats:

Links:

LOCUS SPSPSA2 1620 bp DNA BCT 14-OCT-1997

DEFINITION Streptococcus pneumoniae SIgA binding.

ACCESSION AJ002054

NID g2576330

VERSION AJ002054.1 GI:2576330

KEYWORDS SpsA protein.

SOURCE Streptococcus pneumoniae.

ORGANISM Streptococcus pneumoniae

Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
Streptococcus.

REFERENCE 1 (bases 1 to 1620)

AUTHORS Hammerschmidt,S.

TITLE Direct Submission

JOURNAL Submitted (13-OCT-1997) Hammerschmidt S., Microbiology, Devison  
Microbial Pathogenesis, National Research Centre for Biotechnology,  
Spielmannstrasse 7, 38106 Braunschweig, GERMANY

REFERENCE 2 (bases 1 to 1620)

AUTHORS Hammerschmidt,S., Talay,S.R., Brandtzaeg,P. and Chhatwal,G.S.

TITLE SpsA, a novel pneumococcal surface protein with specific binding to  
secretory immunoglobulin A and secretory component

JOURNAL Mol. Microbiol. 25 (6), 1113-1124 (1997)

MEDLINE 98010350

FEATURES Location/Qualifiers

source 1..1620

/organism="Streptococcus pneumoniae"

/strain="type 2"

/db\_xref="taxon:1313"

CDS 1..1620

/function="IgA binding protein"

/codon\_start=1

/transl\_table=11

/product="SpsA protein"

/protein\_id="CAA05158.1"

/db\_xref="PID:e354783"

/db\_xref="PID:g2576331"

/db\_xref="GI:2576331"

/db\_xref="SPTREMBL:O33741"

/translation="MFASKSERKVHYSIRKFSIGVASVAVASLVMGSVVHATENEGST

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ELNVLEEKSKDELPSEIKAKLDAAFEKFKKDTLKPGEKVAEAKKKVEEAKKKAE  
DQKE

EDRRNYPTNTYKTLLELEIAEFDVKVKEAELELVKEEAKEFRNEGTIKQAKEKVES  
KKA

EATRLENIKTDRKKAEEEEAKRKAAEEDKVKEKPAEQQPAPATQPEKPAPKPEK  
PAEQ

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WYFYN

TDGSMATGWLQNNGSWYYLNANGAMATGWLQNNGSWYYLNANGSMATGW  
LQNNGSWYY

LNANGAMATGWLQYNGSWYYLNSNGAMATGWLQYNGSWYYLNANGDMAT  
GWLQNNGSW

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repeat\_region 961..1564

/rpt\_type=DIRECT

BASE COUNT 625 a 294 c 370 g 331 t

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61 gttagctagtg tagctgttgc cagtcttgtt atgggaagtg tggttcatgc gacagagaac  
121 gagggaagta cccaagcagc cactcttct aatatggcaa agacagaaca taggaaagct  
181 gctaaacaag tcgtcgatga atatatagaa aaaatgttga gggagattca actagataga  
241 agaaaacata cccaaaatgt cgccttaaac ataaagtga gcgcaattaa aacgaagtat  
301 ttgcgtgaat taaatgtttt agaagagaag tcgaaagatg agttgccgct agaaataaaa  
361 gcaaagtag acgcagcttt tgagaagttt aaaaaagata cattgaaacc aggagaaaa  
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541 ttcgatgtga aagttaaaga agcggagctt gaactagtaa aagaggaagc taaagaattt  
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661 acaaggtagt aaaacatcaa gacagatcgt aaaaaagcag aagaagaagc taaacgaaaa  
721 gcagcagaag aagataaagt taaagaaaaa ccagctgaac aaccacaacc agcgccggct  
781 actcaaccag aaaaaccagc tccaaaacca gagaagccag ctgaacaacc aaaagcagaa  
841 aaaacagatg atcaacaagc tgaagaagac tatgctcgta gatcagaaga agaataaat  
901 cgcttgactc aacagcaacc gccaaaaact gaaaaaccag cacaaccatc tactccaaaa  
961 acagggtgga aacaagaaaa cggtagtggt tacttctaca atactgatgg ttaattggca  
1021 acaggatggc tccaaaacaa cggtagtggt tactatctaa acgctaattg tgctatggcg  
1081 acaggatggc tccaaaacaa tggtagtggt tactatctaa acgctaattg ttaattggca  
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the above report in format

[illegible]

Fig. 9

Other Formats:

Links:

LOCUS CAA05159 581 aa BCT 14-OCT-1997

DEFINITION SpsA protein.

ACCESSION CAA05159

PID g2576333

VERSION CAA05159.1 GI:2576333

DBSOURCE embl locus SPSPSA47, accession AJ002055.1

KEYWORDS

SOURCE Streptococcus pneumoniae.

ORGANISM Streptococcus pneumoniae

Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
Streptococcus.

REFERENCE 1 (residues 1 to 581)

AUTHORS Hammerschmidt,S.

TITLE Direct Submission

JOURNAL Submitted (13-OCT-1997) Hammerschmidt S., Microbiology, Devison  
Microbial Pathogenesis, National Research Centre for Biotechnology,  
Spielmannstrasse 7, 38106 Braunschweig, GERMANY

REFERENCE 2 (residues 1 to 581)

AUTHORS Hammerschmidt,S., Talay,S.R., Brandtzaeg,P. and Chhatwal,G.S.

TITLE SpsA, a novel pneumococcal surface protein with specific binding to  
secretory immunoglobulin A and secretory component

JOURNAL Mol. Microbiol. 25 (6), 1113-1124 (1997)

MEDLINE 98010350

FEATURES Location/Qualifiers

source 1..581  
/organism="Streptococcus pneumoniae"  
/strain="type 47"  
/db\_xref="taxon:1313"

Protein 1..581  
/function="IgA binding protein"  
/product="SpsA protein"

CDS 1..581  
/db\_xref="SPTREMBL:O33742"  
/coded\_by="AJ002055.1:1..1746"  
/transl\_table=11

ORIGIN

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61 akqvvdieyie kmlreiqldr rkhtqnvaln iklsaiktky lrelnvleek skdelpseik  
121 akldaafekf kkdtkpgek vaeakkkvee akkkaedqke edrrnyptnt yktleleia  
181 fdvkvkeael elvkeeakes megitikqak ekveskkaea trleniktdr kkaeeekrk  
241 adaklkeanv atsdqgkpkg rakrgvpge atpdkkenda kssdssvgee tlpssslksg  
301 kkvaeeakkv eeaekakdq keedrrnypt ntyktldlei aedsvkvkea elelvkeeak  
361 eprdeekikq akakveskka eatrlenikt drkkaeeek rkaeedkvk ekpaeqpqpa

421 patqpekpap kpekpaepk aektdqae edyarrsee ynriqqppp ktekpaqpf  
481 pktgwkqeng mwyfyntdgs matgwlqyng swyylnangd matgwkdg twyyleasga  
541 mkasqwfks dkwyvngsg alavnttdg ygvnangewv n

//

Fig. 9 (cont'd)

the above report in format

421 patqpekpap kpekpaepk aektdqae edyarrsee ynriqqppp ktekpaqpf  
481 pktgwkqeng mwyfyntdgs matgwlqyng swyylnangd matgwkdg twyyleasga  
541 mkasqwfks dkwyvngsg alavnttdg ygvnangewv n

Fig. 9 (cont'd)

page 3

Other Formats:

Links:

LOCUS SPSPSA47 1746 bp DNA BCT 14-OCT-1997

DEFINITION Streptococcus pneumoniae SIgA binding.

ACCESSION AJ002055

NID g2576332

VERSION AJ002055.1 GI:2576332

KEYWORDS SpsA protein.

SOURCE Streptococcus pneumoniae.

ORGANISM Streptococcus pneumoniae

Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
Streptococcus.

REFERENCE 1 (bases 1 to 1746)

AUTHORS Hammerschmidt,S.

TITLE Direct Submission

JOURNAL Submitted (13-OCT-1997) Hammerschmidt S., Microbiology, Division  
Microbial Pathogenesis, National Research Centre for Biotechnology,  
Spielmannstrasse 7, 38106 Braunschweig, GERMANY

REFERENCE 2 (bases 1 to 1746)

AUTHORS Hammerschmidt,S., Talay,S.R., Brandtzaeg,P. and Chhatwal,G.S.

TITLE SpsA, a novel pneumococcal surface protein with specific binding to  
secretory immunoglobulin A and secretory component

JOURNAL Mol. Microbiol. 25 (6), 1113-1124 (1997)

MEDLINE 98010350

FEATURES Location/Qualifiers

source 1..1746

/organism="Streptococcus pneumoniae"

/strain="type 47"

/db\_xref="taxon:1313"

CDS 1..1746

/function="IgA binding protein"

/codon\_start=1

/transl\_table=11

/product="SpsA protein"

/protein\_id="CAA05159.1"

/db\_xref="PID:e354769"

/db\_xref="PID:g2576333"

/db\_xref="GI:2576333"

/db\_xref="SPTREMBL:O33742"

/translation="MFASKSERKVHYSIRKFSIGVASVAVASLVMGSVVHATENEGST

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KYLR

Fig. 9 (cont'd)

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KKA

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NTYK

TLDLEIAESDVKVKEAELELVKEEAKEPRDEEKIKQAKAKVESKKA EATRLNIK  
TDR

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DQAE

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repeat\_region 1447..1690

/rpt\_type=DIRECT

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181 gctaaacaag tcgtcgatga atatataaaa aaaatgttga gggagattca actagataga  
241 agaaaacata cccaaaatgt cgccttaaac ataaagtga gcgcaattaa aacgaagtat  
301 ttgcgtgaat taaatgttt agaagagaag tcgaaagtgc agttgccgtc agaaataaaa  
361 gcaaagttag acgcagcttt tgagaagttt aaaaaagata cattgaaacc aggagaaaag  
421 gtagcagaag ctaagaagaa ggttgaagaa gctaagaaaa aagccgagga tcaaaaagaa  
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601 cgaacagagg gcacaattaa gcaagcaaaa gagaagttg agagtaaaaa agctgaggct  
661 acaaggttag aaaacatcaa gacagatcgt aaaaaagcag aagaagaagc taaacgaaaa  
721 gcagatgcta agttgaagga agctaagtga gcgacttcag atcaaggtaa accaaagggg  
781 cgggcaaaac gaggagttcc tggagagcta gcaacacgtg ataaaaaaga aatgatgcg  
841 aagtcttcag atttagcgt aggtgaagaa actcttccaa gctcatccct gaaatcagga  
901 aaaaaggtga cagaagctga gaagaaggtt gaagaagctg agaaaaaagc caaggatcaa  
961 aaagaagaag atcgccgtaa ttaccaacc aatactaca aaacgcttga ccttgaaatt

1021 gctgagtcgc agtgaagaagt taaagaagcg gagcttgaac tagtaaaaaa ggaagctaag  
1081 gaacctcgag acgagggaaa aattaagcaa gcaaaaagcga aagttagag taaaaaagct  
1141 gaggtacaa ggttagaaaa catcaagaca gatcgtaaaa aagcagaaga agaagctaaa  
1201 cgaaaagcag cagaagaaga taaagttaaa gaaaaccag ctgaacaacc acaaccagcg  
1261 ccggctactc aaccagaaaa accagctcca aaaccagaga agccagctga acaacaaaa  
1321 gcgaaaaaaa catgatgata acaagctgaa gaagactatg ctctgatgc agaagaagaa  
1381 tataatcgct tgattcaaca gcaaccgcca aaaactgaaa aaccagcaca accatttact  
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1501 atggcaacg gatggtcca atacaacggt tcatggtatt acctcaacgc taatggtgat  
1561 atggcgacag gttgggtgaa agatggagat acctggtact atctgaagc atcaggtgct  
1621 atgaaagcaa gccaatggtt caaagtatca gataaatggt actatgtcaa tggctcaggt  
1681 gcccttcgac tcaacacaac tggatagtcg tatggagtc atgccaatgg tgaatgggta  
1741 aactaa

Fig. 9 (cont'd)

the above report in format

Fig. 90

ther Formats:

Links:

LOCUS AAB70838 663 aa BCT 16-SEP-1997

DEFINITION choline binding protein A.

ACCESSION AAB70838

PID g2425109

VERSION AAB70838.1 GI:2425109

DBSOURCE locus AF019904 accession AF019904.1

KEYWORDS

SOURCE Streptococcus pneumoniae.

ORGANISM Streptococcus pneumoniae

Eubacteria; Firmicutes; Low G+C gram-positive bacteria;

Streptococcaceae; Streptococcus.

REFERENCE 1 (residues 1 to 663)

AUTHORS Rosenow,C., Ryan,P., Weiser,J.N., Johnson,S., Fontan,P.,  
Ortqvist,A. and Masure,H.R.TITLE Contribution of novel choline-binding proteins to adherence,  
colonization and immunogenicity of Streptococcus pneumoniae

JOURNAL Mol. Microbiol. (1997) In press

REFERENCE 2 (residues 1 to 663)

AUTHORS Rosenow,C., Ryan,P., Weiser,J.N., Johnson,S., Fontan,P.,  
Ortqvist,A. and Masure,H.R.

TITLE Direct Submission

JOURNAL Submitted (18-AUG-1997) Infectious Diseases, St. Jude Children's  
Research Hospital, 322 North Lauderdale, Memphis, TN 38105, USA

COMMENT Method: conceptual translation supplied by author.

FEATURES Location/Qualifiers

source 1..663

/organism="Streptococcus pneumoniae"

/strain="R6x"

/db\_xref="taxon:1313"

Protein &lt;1..663

/product="choline binding protein A"

/name="CbpA"

CDS 1..663

/gene="cbpA"

/coded\_by="AF019904.1:&lt;1..1992"

/transl\_table=11

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121 keedrrnypt ntyktlelei aefdvkykea elelvkeeak esrnegtikq akekveskka  
181 eatrlenikt drkkaeeak rkadalkea nvatsdggkp kgrakrgvpg elatpdkken  
241 dakssdssvg eetlpssslk sgkkvaeak kveeaekkak dqkeedrny ptntyktldl  
301 eiaesdvkvk eaelelvkee akeprdeeki kqakakvesk kaeatrleni kdrkkaeee

Page 2

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## Other Formats:

## Links:

LOCUS AF019904 2480 bp DNA BCT 22-SEP-1997

DEFINITION Streptococcus pneumoniae choline binding protein A (cbpA) gene,  
partial cds.

ACCESSION AF019904

NID g2425108

VERSION AF019904.1 GI:2425108

## KEYWORDS

SOURCE Streptococcus pneumoniae.

ORGANISM Streptococcus pneumoniae

Eubacteria; Firmicutes; Low G+C gram-positive bacteria;

Streptococcaceae; Streptococcus.

REFERENCE 1 (bases 1 to 2480)

AUTHORS Rosenow,C., Ryan,P., Weiser,J.N., Johnson,S., Fontan,P.,  
Ortvist,A. and Masure,H.R.

TITLE Contribution of novel choline-binding proteins to adherence,  
colonization and immunogenicity of Streptococcus pneumoniae

JOURNAL Mol. Microbiol. (1997) In press

REFERENCE 2 (bases 1 to 2480)

AUTHORS Rosenow,C., Ryan,P., Weiser,J.N., Johnson,S., Fontan,P.,  
Ortvist,A. and Masure,H.R.

TITLE Direct Submission

JOURNAL Submitted (18-AUG-1997) Infectious Diseases, St. Jude Children's  
Research Hospital, 322 North Lauderdale, Memphis, TN 38105, USA

## FEATURES Location/Qualifiers

source 1..2480

/organism="Streptococcus pneumoniae"

/strain="R6x"

/db\_xref="taxon:1313"

gene <1..1992

/gene="cbpA"

CDS <1..1992

/gene="cbpA"

/note="CbpA"

/codon\_start=1

/transl\_table=11

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/protein\_id="AAB70838.1"

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Fig 10 (c) (l)

page 4

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KEEAK

ESRNEGTIKQAKEKVESKKAETRLENIKTDRKKAEEEEAKRKADAKLKEANVAT  
SDQG

KPKGRAKRGVPGELATPDKKENDAKSSDSSVGEETLPSSSLKSGKKVAEAEKKV  
EEAE

KKAKDQKEEDRRNYPTNTYKTLDEIAESDVKVKEAELELVKEEAKEPRDEEKI  
KQAK

AKVESKKAETRLENIKTDRKKAEEEEAKRKAAEEDKVKEKPAEQQPAPATQPE  
KPAE

KPEKPAEQPKAEKTDDQQAEDYARRSEEEYNRLTQQQPPKTEKPAQPSTPKTG  
WKQE

NGMWYFYNTDGSMATGWLQNNGSWYYLNANGAMATGWLQNNGSWYYLNA  
NGSMATGWL

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NANGDMATG

WLQNNGSWYYLNANGDMATGWLQYNGSWYYLNANGDMATGWVKDGDWTWY  
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ASQWFKVSDKWYYVNGSGALAVNTTVDGYGVNANGEWVN"

BASE COUNT 933 a 452 c 575 g 520 t

ORIGIN

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121 gatagaagaa aacataccca aaatgtcgcc ttaacataa agttgagcgc aattaaaacg  
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241 ataaaagcaa agttagacgc agcttttgag aagtttaaaa aagatacatt gaaaccagga  
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481 gaatctgcaa acgagggcac aattaagcaa gcaaaagaga aagttgagag taaaaaagct  
541 gaggtacaa ggtagaaaa catcaagaca gatcgtaaaa aagcagaaga agaagctaaa  
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661 aagggggcggg caaaacgagg agttcttgga gagctagcaa cacctgataa aaaagaaaat  
721 gatcggaagt ctcagattc tagcgtaggt gaagaaactc ttcaaagtc atccctgaaa

Fig 10 (cont'd)

Page 5

781 tcaggaaaa aggtagcaga agctgagaag aaggttgaag aagctgagaa aaaagccaag  
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961 gctaaggaac ctcgagacga ggaaaaaatt aagcaagcaa aagcgaaagt tgagagtaaa  
1021 aaagctgagg ctacaagggt agaaaacatc aagacagatc gtaaaaaagc agaagaagaa  
1081 gctaaacgaa aagcagcaga agaagataaa gtaaaagaaa aaccagctga acaaccacaa  
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2161 tgatgaggaa agaattggcg cattcaagag actctttaag agagttacgg gttttaaact  
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2281 ggctccacgg agtttggcag cgccagatgt tccacggaga tagtgaggag cgaggccgag  
2341 gaattcacga actgcgacgt ttctccttt gaggttaac aatcgttca agtgttcgta  
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//

the above report in format

Fig. 11

Other Formats:

Links:

LOCUS AAD00184 929 aa BCT 07-OCT-1996

DEFINITION surface protein C.

ACCESSION AAD00184

PID g4097980

VERSION AAD00184.1 GI:4097980

DBSOURCE locus SPU72655 accession U72655.1

KEYWORDS

SOURCE Streptococcus pneumoniae.

ORGANISM Streptococcus pneumoniae

Eubacteria; Firmicutes; Low G+C gram-positive bacteria;

Streptococcaceae; Streptococcus.

REFERENCE 1 (residues 1 to 929)

AUTHORS Brooks-Walter,A., Tart,R.C., Briles,D.E. and Hollingshead,S.K.

TITLE The pspC gene encodes a second pneumococcal surface protein  
homologous to the protection-eliciting PspA protein of  
Streptococcus pneumoniae

JOURNAL Unpublished

REFERENCE 2 (residues 1 to 929)

AUTHORS Brooks-Walter,A., Tart,R.C., Briles,D.E. and Hollingshead,S.K.

TITLE Direct Submission

JOURNAL Submitted (26-SEP-1996) Microbiology, University of Alabama at  
Birmingham, 19th Street South, Box 10, Birmingham, AL 35294-2170,  
USA

FEATURES Location/Qualifiers

source 1..929

/organism="Streptococcus pneumoniae"

/strain="EF6796"

/db\_xref="taxon:1313"

Protein 1..929

/product="surface protein C"

CDS 1..929

/gene="pspC"

/coded\_by="U72655.1:319..3108"

/transl\_table=11

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 181 eiaesdvevk kaelelvkvk akesqdeeki kqaeavesk qaeatrkki ktdreeakrk  
 241 adaklkeave knvatseqdk pkrakrgvs gelatpdkke ndakssdsv geetlpspsl  
 301 nmanesqteh rkdvdeyikk mlseiqlrr khtqvnlni klsaiktlyl yelsvlkens  
 361 kkeelstktk aeltaafeqf kkdtklpekk vaeaeekvee akkakakdqke edrnyptnt  
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//

[illegible]

Fig. 15 (cont'd)

Links:

NLTVTSSGQDISKKYADEVESHLESILKDVKKNLKKVQHTQNVGLITKLSEIKKK  
YLY

Fig. 1 (cont'd)

Page 4

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EVE

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ELATP

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KVA

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ANES

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BASE COUNT 1326 a 591 c 755 g 790 t 1 others

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301 atatagaagg aaataaacat gtttgcatca aaaagcgaaa gaaaagtaca ttattcaatt  
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541 aaaaaaaatt tgaaaaaagt tcaacatacc caaatgtcg gcttaattac aaagttgagc  
601 gaaattaaaa agaagtattt gtatgactta aaagttaatg tttatcggg agctgagttg  
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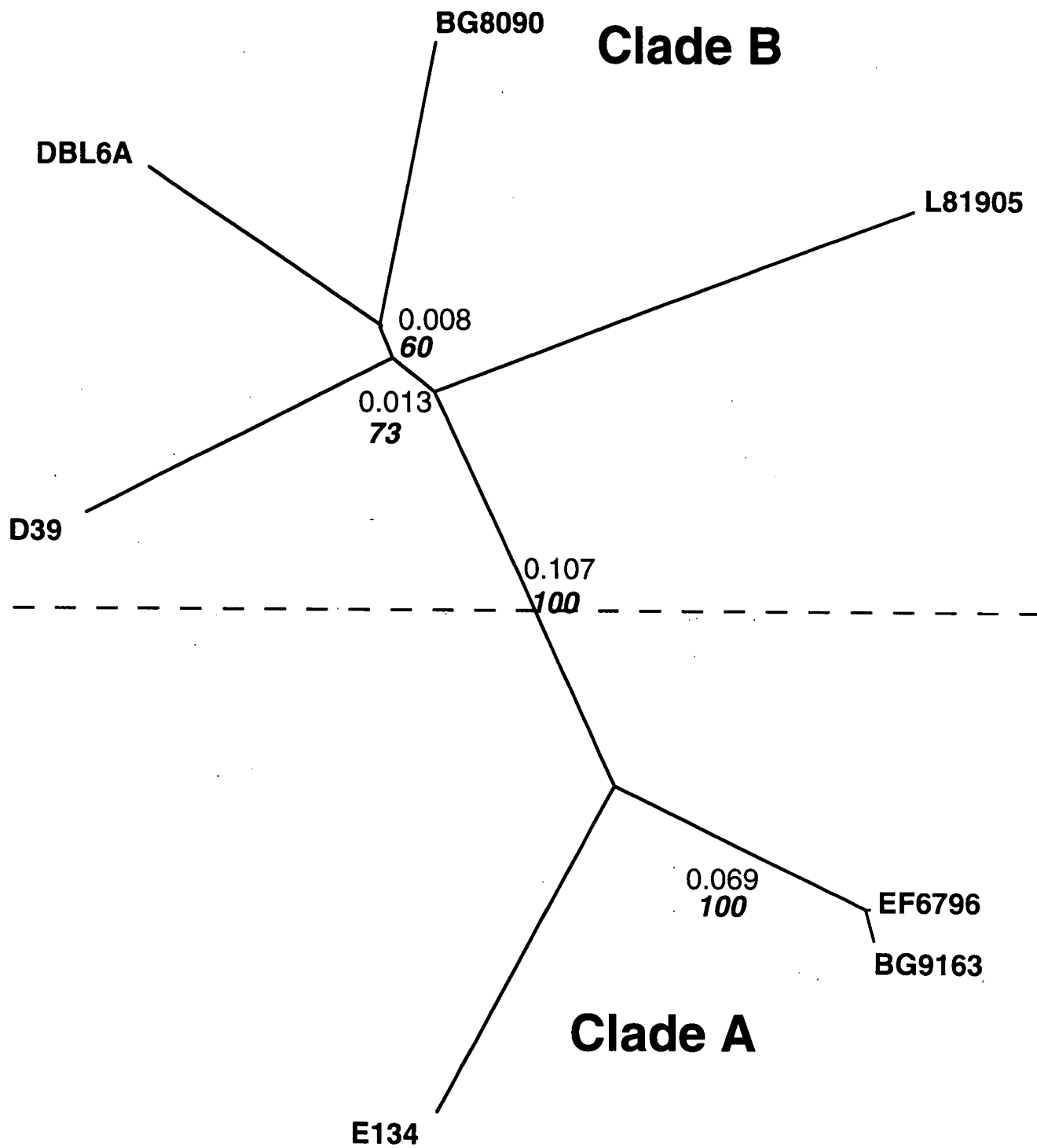


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//

the above report in format

FIG. 12



— 0.05 changes

UAB pspc align.fasta Formatted Alignments

Fig. 13

# UAB PspC Sequences

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BG9163	MFASKSERKVVHYSIRKFSIGVAAVAASLFLGGVVAHAEVGR--SGNNLTVTSTSGQDISKKYADEVES-						
E134	MFASKSERKVVHYSIRKFSIGVAAVAASLFLGGVVAHAEVGR--SGNNLTVTSTSGQDISKKYADEVES-						
D39	MFASKSERKVVHYSIRKFSIGVAAVAASLFLGGVVAHAEVGR--SGNNLTVTSTSGQDISKKYADEVES-						
DBL6A	MFASKSERKVVHYSIRKFSIGVAAVAASLFLGGVVAHAEVGR--SGNNLTVTSTSGQDISKKYADEVES-						
BG8090	MFASKSERKVVHYSIRKFSIGVAAVAASLFLGGVVAHAEVGR--SGNNLTVTSTSGQDISKKYADEVES-						
L81905	MFASKSERKVVHYSIRKFSIGVAAVAASLFLGGVVAHAEVGR--SGNNLTVTSTSGQDISKKYADEVES-						
EF6796	80	90	100	110	120	130	140
BG9163	HLKSLKDVKKNLKQVQ--HTQNVGLITKLSBTKKVLVDLKVNVLSAEELTSKTK						
E134	HLKSLKDVKKNLKQVQ--HTQNVGLITKLSBTKKVLVDLKVNVLSAEELTSKTK						
D39	HLKSLKDVKKNLKQVQ--HTQNVGLITKLSBTKKVLVDLKVNVLSAEELTSKTK						
DBL6A	HLKSLKDVKKNLKQVQ--HTQNVGLITKLSBTKKVLVDLKVNVLSAEELTSKTK						
BG8090	HLKSLKDVKKNLKQVQ--HTQNVGLITKLSBTKKVLVDLKVNVLSAEELTSKTK						
L81905	HLKSLKDVKKNLKQVQ--HTQNVGLITKLSBTKKVLVDLKVNVLSAEELTSKTK						
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E134	ETKEKLTATTTTQFQKKTLL--PTEPEKKVAAEQKKVEEAKKKAEDDQKEKDRR						
D39	ETKEKLTATTTTQFQKKTLL--PTEPEKKVAAEQKKVEEAKKKAEDDQKEKDRR						
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BG8090	ETKEKLTATTTTQFQKKTLL--PTEPEKKVAAEQKKVEEAKKKAEDDQKEKDRR						
L81905	ETKEKLTATTTTQFQKKTLL--PTEPEKKVAAEQKKVEEAKKKAEDDQKEKDRR						
EF6796	220	230	240	250	260	270	280
BG9163	NYPTTITTYKTLLHLEIAESDVVKKABELELVKKAKESQDEEKKIKQAEAEVSKQAEATRLKIKTDR						
E134	NYPTTITTYKTLLHLEIAESDVVKKABELELVKKAKESQDEEKKIKQAEAEVSKQAEATRLKIKTDR						
D39	NYPTTITTYKTLLHLEIAESDVVKKABELELVKKAKESQDEEKKIKQAEAEVSKQAEATRLKIKTDR						
DBL6A	NYPTTITTYKTLLHLEIAESDVVKKABELELVKKAKESQDEEKKIKQAEAEVSKQAEATRLKIKTDR						
BG8090	NYPTTITTYKTLLHLEIAESDVVKKABELELVKKAKESQDEEKKIKQAEAEVSKQAEATRLKIKTDR						
L81905	NYPTTITTYKTLLHLEIAESDVVKKABELELVKKAKESQDEEKKIKQAEAEVSKQAEATRLKIKTDR						
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E134	NYPTTITTYKTLLHLEIAESDVVKKABELELVKKAKESQDEEKKIKQAEAEVSKQAEATRLKIKTDR						
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DBL6A	NYPTTITTYKTLLHLEIAESDVVKKABELELVKKAKESQDEEKKIKQAEAEVSKQAEATRLKIKTDR						
BG8090	NYPTTITTYKTLLHLEIAESDVVKKABELELVKKAKESQDEEKKIKQAEAEVSKQAEATRLKIKTDR						
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UAB PSPC align. last

[illegible]

FIG. 13 (cont'd)

[illegible]

780

P E K P A P A P K P E T P E T

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BG9163  
E134  
D39  
DBL6A  
BG8090  
L81905

FIG 13 (cont'd)

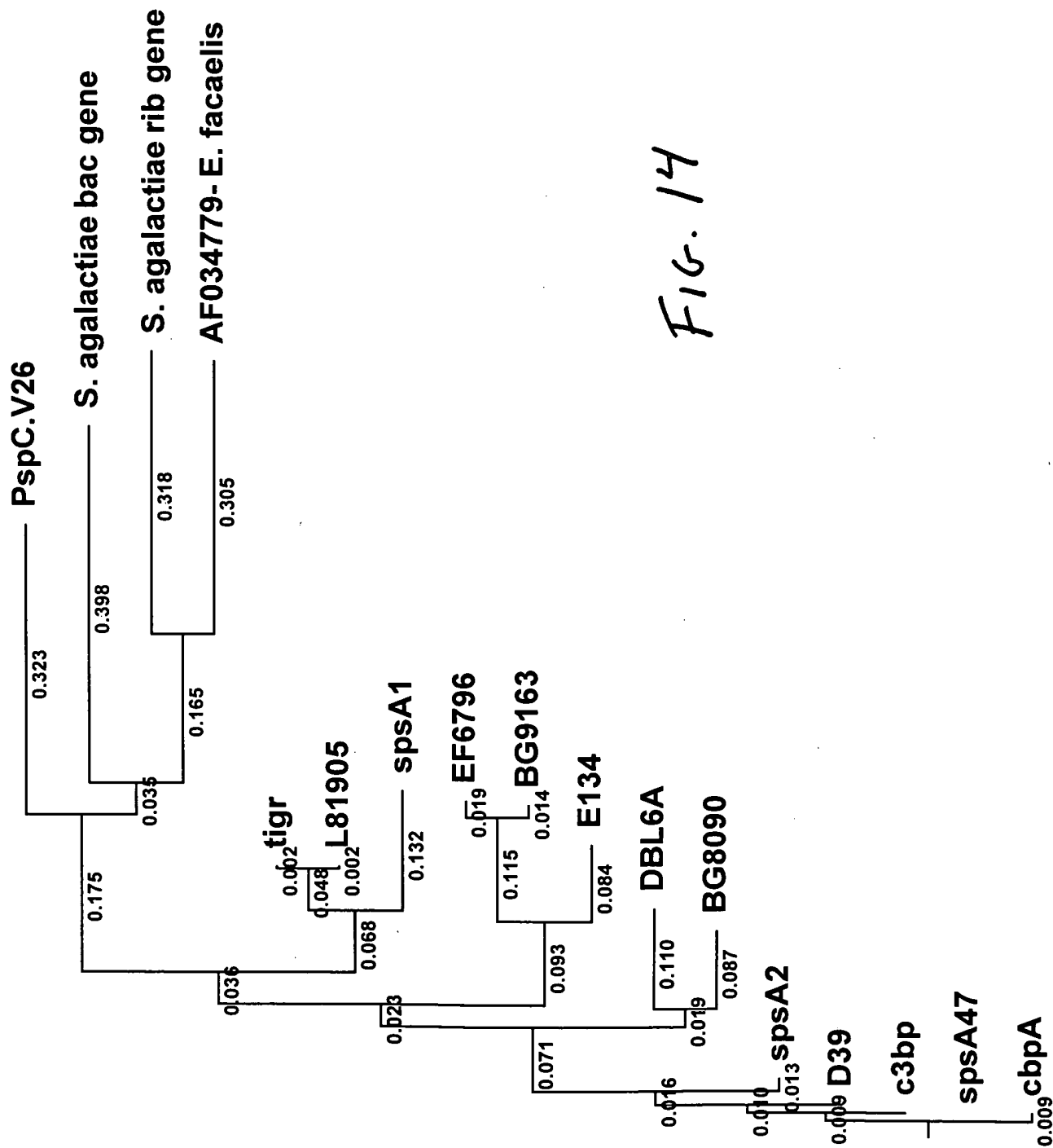


Fig. 14

Thomas Kowalski : PspC.V26

LOCUS PSPC.V26 730 AA PROT SYN ~~33-11-1999~~  
 DEFINITION Streptococcus pneumoniae PspC protein from strain V26

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES Location/Qualifiers

PROPEP &lt;1..731


/note="3 to 2349 of V26.pspC (translated)"

ORIGIN -

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 121 KEPELTKKLA EAEKKAKDQK EEDHRNYPTN TYKTIELEIA EAEVGVAKAE LELAQAQVQI  
 181 PQDTEKINAA KAKVEAAKSN VKKLEIKSD IEKTYLYKLD NSTKETPKSR VRRNSPQVGD  
 241 SRELKETIDK AKETLSTYMV TRLTCLDPSV FWFADLLMDA KKVVEEYTK LEDASDKKSV  
 301 EDLRKEAEGK IESLIVTHQN REKENQPAPQ PGGQAGGSMV VPPVTQTTPS TSQSPGQKAT  
 361 EAEKKKLQDL IRQFQEALNK LDDETKTVPD GAKLTGEAGK AYNETRTRYAK EVVDKSKLL  
 421 SQTAVTMDL AMQLTKLND MSKLKEAKAK LVPEVKPQPE NPEPKPQPEG EKPSVPDINQ  
 481 EKEKAKLAIA TYMSKILDDI KKHHLKKEKH HQIVALIKDL DKLRKQALSE IDNVNTKVEI  
 541 ENTVHKVFAD MDTVVTKFQK GLIQNTQVP EAQRAQRYQR FQIHQKAPDT PQVPEAPKSP  
 601 EVPKVPEAPK APDTPQVPEA PKSPEVPKVS DTPKAPDTPQ VPEAPKSPEV PKVPEAPKAP  
 661 DTPQVPEAPK SPEVPKVPDT PKAPDTPQVP EAPKAPDTPQ IPEAPAPETP APAPEAPKTG  
 721 WKQENGMWKG

//

Fig. 15

LOCUS V26DNA.PSP 2349 BP SS-DNA SYN 

DEFINITION Streptococcus pneumoniae PspC gene from strain V26

ACCESSION -

KEYWORDS -

SOURCE -

BASE COUNT 937 A 457 C 505 G 450 T 0 OTHER

ORIGIN -

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181 GAAAAGTACA TTATTCAATT CGTAAATTTA GTATTGGAGT AGCTAGTGTA GTAGTTGCTA  
241 GTTTGTCTT AGGAGGAGTA GTTCACGCAG AAGAGGTTAG AAGAGGGAAT AACCTCACGG  
301 TTACATCTAG TGGGGATGAA GTCGAGTCGC ATTATCAAAG TATATTGGAG AAGGTCAGAA  
361 AAAGTTTGA AAAAGATCGA CATACCCAAA ATGTCGACTT AATCAAAAAG TTGCAAGACA  
421 TTAAGAGAAC GTATTTGTAT AATTTAAAG AGAAGCCGGA AGCTGAGTTG ACGTCAAAAA  
481 CAAATAAAGA GTTAGACGCA GCTTTTGAGA AGTTTAAAA AGAACCGAGAA CTTACTAAAA  
541 AATTAGCAGA AGCTGAGAAA AAAGCCCAAGG ATCAAAAAGA AGAAGATCAC CGTAACCTACC  
601 CAACCAATAC TTACAAAACA ATCGAACTGG AAATTGCGGA AGCAGAAGTA GGGGTCGCCA  
661 AGGCAGAGCT TGAGCTTGCA CAAGCTCAAG TCCAAATACC TCAAGATACT GAGAAAATTA  
721 ATGCTGCTAA AGCTAAAGTA GAAGCTGCTA AAAGTAATGT TAAAAACTA GAAAAAATTA  
781 AATCAGATAT TGA AAAAACG TATTTGTATA AATTAGATAA CTC AACCCAA GAAACGCCAA  
841 AATCTAGAGT CGGAAGAAAT TCTCCGCAAG TAGGCGATT C GAGAGAACTT AAGGAAACGA  
901 TAGACAAAGC GAAAGAAACT CTGTCTACCT ATATGGTAA C TCGTTTAAACG AAGCTGGATC  
961 CATCTGTTT TTGGTTTGCA GATCTTCTTA TGGATGCTAA GAAAGTTGTG GAAGAATACA  
1021 AGACAAAATT AGAGGATGCT TCAGATAAAA AATCGGTAGA AGACTTGCGA AAGGAAGCAG  
1081 AAGGAAAAAT AGAGTCTCTT ATCGTGACTC ACCAAATAG AGAAAAAGAA AACCAACCAG  
1141 CACCCCAACC AGGAGGACAA GCAGGTGGT CAATGGTTGT ACCACCGGTG ACGCAAACAC  
1201 CTCCATCAAC TTCCCAAAGT CCAGGACAAA AGCGACCGA AGCTGAAAAG AAAAAGTTAC  
1261 AAGACTTGAT TCGTCAATTC CAAGAAGCCT TGAACAACT AGACGATGAA ACAAGACTG  
1321 TTCCAGATGG GGCTAAACTC ACAGGAGAAG CTGGAAGAGC CTATAATGAG ACTAGAAGTT  
1381 ATGCGAAAAGA AGTTGTTGAC AAGAGCAAGA AGCTTCTATC ACAGACAGCA GTGACAAATG  
1441 ATGAATTGGC AATGCAATTA ACCAAATTGA ACGATGCCAT GTCTAAATTG AAAGAAGCTA  
1501 AAGCGAAATT GGTACCAGAG GTTAAACCAC AGCCGGAAA CCCAGAGCCA AACCCACAAC  
1561 CAGAGGGTGA GAAACCAAGC GTACCAGATA TTAATCAGGA GAAAGAAAA GCTAAACTTG  
1621 CTATAGCAAC ATACATGAGC AAGATTTTAG ATGATATAA GAAACATCAT CTGAAGAAAG  
1681 AAAACATCA TCAGATTGTT GCTCTTATTA AGGACCTTGA TAACTTAGA AAGCAAGCAC  
1741 TTTCTGAAT TGATAATGTA AATACCAAAG TAGAAATTGA GAATACAGTC CACAAGGTAT  
1801 TTGCAGACAT GGATACGGT GTTACTAAAT TCCAAAAGG CTTAATTGAG AACACCCGC  
1861 AGGTTCCAGA AGCCCAAAGA GCCCAGAGGT ACCAAAGGTT TCAGATACAC CAAAAGGCTC

Fig. 15 (cont'd)



1921 CGGACACACC GCAGGTTCCA GAAGCACCAA AGAGCCCAGA GTACCAAAG GTTCCAGAAG  
1981 CACCAAAGGC TCCGGACACA CCGCAAGTTC CGGAAGCACC AAAGAGCCCA GAGGTACCAA  
2041 AGGTTTCAGA TACACCAAAG GCTCCGGACA CACCGCAGGT TCCAGAAGCA CCAAAGAGCC  
2101 CAGAGGTACC AAAGGTTCCA GAAGCACCAA AGGCTCCGA CACACCGCAA GTTCCGGAAG  
2161 CACCAAAGAG CCCAGAGGTA CCAAGGTTT CAGATACACC AAAGGCTCCG GACACACCGC  
2221 AGGTTCCAGA AGCACCAGG GCTCCAGACA CACCGCAAAT TCCGGAAGCA CCAGCTCCAG  
2281 AAAGTCCGGC TCCAGCTCCA GAAGCTCCA AAACAGGCTG GAAACAAGAA AACGGTATGT  
2341 GGAAGGGCG

//

Fig. 15 (cont'd)

Fig. 16

LOCUS E134.DNA 2405 BP SS-DNA SYN ~~XXXXXXXXXX~~  
DEFINITION -  
ACCESSION -  
KEYWORDS -  
SOURCE -  
FEATURES Location/Qualifiers  
CDS 187..2405  
BASE COUNT 1046 A 386 C 505 G 468 T 0 OTHER  
ORIGIN -


1 CGGCCGCCAG TGTGATGGAT ATCTGCAGAA TTCGCCCTTC GACGAATAGC TGAAGAGGAA  
61 AAGCTATTAC ATGAAGTTAT AATCCCAAAT GGAAGCATAA AGAGATAAAT ACAAATTCG  
121 ATTTATATAC AGTTCATATT GAAGTGATAT AGTAAGGTTA AAGAAAAAAT ATAGAAGGAA  
181 ATAAACATGT TTGCATCAAA AAGCGAAAGA AAAGTACATT ATTCAATTCG TAAATTTAGT  
241 ATTGGAGTAG CTAGTGTAGT AGTTGCTAGT CTTGTTATGG GAAGTGTGGT TCATGCGACG  
301 GAGAATGAGG GAATTACCCA AGTAGCCACT TCTTATAATA AGGCAAATGA AAGTCAGACA  
361 GAACATAGGA AAGCTGCTAA ACAAGTCGAT GAAGATATAA AAAAAATGTT GAGTGAGATC  
421 CAAGAATATA TAAAAAAAT GTTGAGTGAG ATCCAATTAG ATAAAAGAAA ACATACCCAA  
481 AATGTCAACT TAAACAGAAA GTTGAGCGCA ATTCAAACGA AGTATTTGTA TGAATTAAGA  
541 GTTTTAAAG AGAAGTCGAA AAAAGAAGAG TTGACGTCAA AAACAAAAAA AGAGTTAGAC  
601 GCAGCTTTTG AGAAGTTTAA AAAAGAACCA GAACTTACTA AAAAATTAGC AGAAGCTAAA  
661 CAAAAGCCA AGGCTCAAAA AGAAGAAGAT TTCCGTAAC TACCAACCAA TACTTACAAA  
721 ACGCTTGAAC TTGAAATTGC TGAGTTCGAT GTGAAAGTTA AAGAAGCGGA GCTTGAAC TA  
781 GTAAAAGAGG AAGCTAAACC CCGAAACGAG GAAAAAATTA AGCAAGCAAA AGCGAAAGTT  
841 GAGAGTAAAA AAGCTGAGGC TACAAGGTTA GAAGAAATCA AGACAGAACG TAAAAAGCA  
901 GAAGAAGAAG CTAAACGAAA AGCAGAAGAA TCTGAGAAAA AAGCTGCTGA AGCCAAACAA  
961 AAAGTGGATA CTAAAGAGCA AGGTAAACCA AAGAGGCGGG CAAAACGAGG  
AGTTTCTGGA  
1021 GAGCTAGCAA CACCTGATAA AAAAGAAAAT GATGCGAAGT CTTGAGATTC TAGCGTAGGT  
1081 GAAGAACTC TTCCAAGCCC ATCCCTTAAT ATGGCAAATG AAAGTCAGAC AGAACATAGG  
1141 AAAGATGTCG ATGAATATAT AAAAAAATG TTGAGTGAGA TCCAATTAGA TAGAAGAAAA  
1201 CATACCCAAA ATGTCAACTT AACATAAAG TTGAGCGCAA TTAACCGAA GTATTTGTAT  
1261 GAATTAAGTG TTTTAAAGA GAACTCGAAA AAAGAAGAGT TGACGTCAA AACCAAAGCA  
1321 GAGTTAACCG CAGCTTTTGA GCAGTTTAAA AAAGATACAT TGAAACCAGA AAAAAAGGTA  
1381 GCAGAAGCTG AGAAGAAGGT TGAAGAAGCT AAGAAAAAAG CCAAGGATCA  
AAAAGAAGAA  
1441 GATCGCCGTA ACTACCCAAC CAATACTTAC AAAACGCTTG AACTTGAAAT TGCTGAGTCC  
1501 GATGTGAAAG TTA AAAAAGC GGAGCTTGAA CTAGTAAAAG AGGAAGCTAA CGAATCTCGA  
1561 AACGAGGAAA AAATTAAGCA AGCAAAAGAG AAAGTTGAGA GTAAAAAGC TGAGGCTACA  
1621 AGGTTAGAAA AAATCAAGAC AGATCGTAAA AAAGCAGAAG AAGAAGCTAA ACGAAAAGCA  
1681 GAAGAATCTG AGAAAAAGC TGCTGAAGCC AAACAAAAAG TGGATGCTGA AGAATATGCT  
1741 CTTGAAGCTA AAATCGCTGA GTTGAATAT GAAGTTCAGA GACTAGAAAA AGAGCTCAAA  
1801 GAGATTGATG AGTCTGACTC AGAAGATTAT CTTAAAGAAG GCCTCCGTGC TCCTCTTCAA  
1861 TCTAAATTGG ATACCAAAAA AGCTAACTA TCAAACTTG AAGAGTTGAG TGATAAGATT  
1921 GATGAGTTAG ACGCTGAAAT TGCAAACTT GAAGTTCAAC TTAAAGATGC TGAAGGAAAC  
1981 AATAATGTAG AAGCTACTT TAAAGAAGGT TTAGAGAAAA CTAAGTCTGA GAAAAAGCT  
2041 GAATTAGAAA AAGCTGAAGC TGACCTTAAG AAAGCAGTTG ATGAGCCAGA AACTCCAGCT  
2101 CCGGCTCCTC AACCAGCTCC AGCTCCAGAA AAACCAGCTG AAAAACCAGC  
TCCAGCTCCA  
2161 GCTCCAGAAA AACCAGCTCC AGCTCCAGAA AAACCAGCTG AAAAACCAGC  
TGAAAAACCA  
2221 GCTGAAGAAC CAGCTGAAAA ACCAGCTCCA GCTCCAGAAA AACCAGCTCC  
AACTCCAGAA  
2281 AAACCAGCTC CAACTCCAGA AACTCCAAAA ACAGGCTGGA AACAAGAAAA  
CGGTATGTGG

2341 TACTTCTACA ATACTGATGG TTCAATGGCA ACAGGCTGGC.TCCAAAACAA TGGTTCATGG  
2401 TACTA

//

*Fig. 16(cont'd)*

2341 TACTTCTACA ATACTGATGG TTCAATGGCA ACAGGCTGGC.TCCAAAACAA TGGTTCATGG  
2401 TACTA

LOCUS D39.DNA 2774 BP SS-DNA SYN   
DEFINITION -  
ACCESSION -  
KEYWORDS -  
SOURCE -  
FEATURES Location/Qualifiers  
CDS 362..2467  
BASE COUNT 1057 A 476 C 615 G 624 T 2 OTHER  
ORIGIN -

*Fig. 17*

1 CCAAGCTATT AGGTGACACT ATAGAATACT CAAGCTATGC ATCAAGCTTA TGCTTGTCAA  
61 TAATCACAAA TATGTAGATC ATATCTTGTT TAGGACAGTA AAACATCCTA ATTACTTTTT  
121 AAATATTCTT CCTGAGTTGA TTGGCTTGAC CTTGTTGAGT CATGCTTATG TGACTTTTGT  
181 TTTAGTTTTT CCAGTTTATG CAGTTATTTT GTATCGACGA ATAGCTGAAG AGGAAAAGCT  
241 ATTACATGAA GTTATAATCC CAAATGGAAG CATAAAGAGA TAAATACAAA ATTCGATTTA  
301 TATACAGTTC ATATTGAAGT AATATAGTAA GGTTAAAGAA AAAATATAGA AGGAAATAAA  
361 CATGTTTGCA TCAAAAAGCG AAAGAAAAGT ACATTATTCA ATTCGTAAAT TTAGTATTGG  
421 AGTAGCTAGT GTAGCTGTTG CCAGTCTTGT TATGGGAAGT GTGGTTCATG CGACAGAGAA  
481 CGAGGGAAGT ACCCAAGCAG CCACCTCTTC TAATATGGCA AAGACAGAAC ATAGGAAAGC  
541 TGCTAAACAA GTCGTCGATG AATATATAGA AAAAATGTTG AGGGAGATTC AACTAGATAG  
601 AAGAAAACAT ACCCAAATG TCGCCTTAAA CATAAAGTTG AGCGCAATTA AAACGAAGTA  
661 TTTGCGTGAA TTAAATGTTT TAGAAGAGAA GTCGAAAGAT GAGTTGCCGT CAGAAATAAA  
721 AGCAAAGTTA GACGCAGCTT TTGAGAAGTT TAAAAAGAT ACATTGAAAC CAGGAGAAAA  
781 GGTAGCAGAA GCTAAGAAGA AGGTTGAAGA AGCTAAGAAA AAAGCCGAGG ATCAAAAAGA  
841 AGAAGATCGT CGTAACTACC CAACCAATAC TTACAAAACG CTTGAACTTG AAATTGCTGA  
901 GTTCGATGTG AAAGTTAAAG AAGCGGAGCT TGAAGTAGTA AAAGAGGAAG CTAAAGAATC  
961 TCGAAACGAG GGCACAATTA AGCAAGCAAA AGAGAAAAGTT GAGAGTAAAA AAGCTGAGGC  
1021 TACAAGGTTA GAAAACATCA AGACAGATCG TAAAAAGCA GAAGAAGAAG CTAACGAAA  
1081 AGCAGATGGT AAGTTGAAGG AAGCTAATGT AGCGACTTCA GATCAAGGTA  
AACCAAAGGG  
1141 GCGGGCAAAA CGAGGAGTTC CTGGAGAGCT AGCAACACCT GATAAAAAAG  
AAATGATGC  
1201 GAAGTCTTCA GATTCTAGCG TAGGTGAAGA AACTCTTCCA AGCTCATCCC TGAAATCAGG  
1261 AAAAAAGGTA GCAGAAGCTG AGAAGAAGGT TGAAGAAGCT GAGAAAAAAG  
CCAAGGATCA  
1321 AAAAGAAGAA GATCGCCGTA ACTACCCAAC CAATACTTAC AAAACGCTTG ACCTTGAAAT  
1381 TGCTGAGTCC GATGTGAAAG TTAAAGAAGC GGAGCTTGAA CTAGTAAAAG  
AGGAAGCTAA  
1441 GGAACCTCGA GACGAGGAAA AAATTAAGCA AGCAAAAGCG AAAGTTGAGA  
GTAAAAAAGC  
1501 TGAGGCTACA AGGTTAGAAA ACATCAAGAC AGATCGTAAA AAAGCAGAAG AAGAAGCTAA  
1561 ACGAAAAGCA GCAGAAGAAG ATAAAGTTAA AGAAAAACCA GCTGAACAAC CACAACCAGC  
1621 GCCGGCTACT CAACCAGAAA AACCAGCTCC AAAACCAGAG AAGCCAGCTG  
ACAACCAAAA  
1681 AGCAGAAAAA ACAGATGATC AACAAGCTGA AGAAGACTAT GCTCGTAGAT CAGAAGAAGA  
1741 ATATAATCGC TTGACTCAAC AGCAACCGCC AAAAAGTAA AAACCAGCAC AACCATCTAC  
1801 TCCAAAAACA GGCTGGAAC AAGAAAACGG TATGTGGTAC TTCTACAATA CTGATGGTTC  
1861 AATGGCAACA GGATGGCTCC AAAACAACGG TTCATGGTAC TATCTAAACG CTAATGGTGC  
1921 TATGGCGACA GGATGGCTCC AAAACAATGG TTCATGGTAC TATCTAAACG CTAATGGTTC  
1981 AATGGCAACA GGATGGCTCC AAAACAATGG TTCATGGTAC TACCTAAACG CTAATGGTGC  
2041 TATGGCGACA GGATGGCTCC AATACAATGG TTCATGGTAC TACCTAAACA  
GCAATGGCGC  
2101 TATGGCGACA GGATGGCTCC AATACAATGG CTCATGGTAC TACCTCAACG  
CTAATGGTGA  
2161 TATGGCGACA GGATGGCTCC AAAACAACGG TTCATGGTAC TACCTCAACG

CTAATGGTGA

2221 TATGGCGACA GGATGGCTCC AATACAACGG TTCATGGTAT TACCTCAACG CTAATGGTGA

2281 TATGGCGACA GGTTGGGTGA AAGATGGANA TACCTGGTAC TATCTTAAAG

CATCAGGTGC

2341 TATGAAAGCA AGCCAATGGT TCAAAGTATC AGATAAATGG TACTATGTCA ATGGCTCAGG

2401 TGCCCTTGCA GTCAACACAA CTGTAGATGG CTATGGAGTC AATGCCAATG

GTGAATGGGT

2461 AAATAAACC TAATATAACT AGTTAATACT GACTTCCTGT AAGAACTTTT TAAAGTATTC

2521 CCTACAAATA CCATATCCTT TCAGTAGATA ATATACCCTT GTAGGAAGTT TAGATTAAAA

2581 AATAACTCTG TAATCTCTAG CCGGATTTAT AGCGCTAGAG ACTACGGAGT TTTTTTGATG

2641 AGGAAAGAAT GCGGGCATTG AAGAGACTCT TTAAGAGAGT TACGGGTTTT AAATAATTAA

2701 GCCTTCTCCA ATTGCAAGAG GGCTTCAATC TCTGCTAGGG TGCTAGCTTG

CGAAATGGCT

2761 CCACGGAGTT TNGC

//

*Fig. 17 (cont'd)*

LOCUS BG9163.DNA 2489 BP SS-DNA

SYN

Fig. 18

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES Location/Qualifiers

CDS 221..2489

BASE COUNT 1026 A 429 C 541 G 493 T 0 OTHER

ORIGIN -

1 GATTGTATAC GACCACTATA GGGCGAATTG GGCCCGACGT CGCATGCTCC CGGCCGCCAT  
61 GGCCGCGGGT ATTCGACGAA TAGCTGAAGA GGAAAAGCTA TTACATGAAG TTATAATCCC  
121 AAATGGAAGC ATAAAGAGAT AAATACAACA TTCGATTTAT ATACAGTTCC TATTGAAGTG  
181 ATATAATAAG GTTAAAGAAA AAATATAGAA GGAAATAAAC ATGTTTGCAT CAAAAGCGA  
241 AAGAAAAGTA CATTATTCAA TTCGTAAATT TAGTATTGGA GTAGCTAGTG TAGCTGTTGC  
301 CAGCTTGTTT TTAGGAGGAG TAGTCCATGC AGAAGGGGTT AGAAGTGGGA ATAACCTCAC  
361 GGTTACATCT AGTGGGCAAG ATATATCGAA GAAGTATGCT GATGAAGTCG AGTCGCATCT  
421 AGAAAGTATA TTGAAGGATG TCAAAAAAAA TTTGAAAAA GTTCAACATA CCCAAATGT  
481 CGGCTTAATT ACAAAGTTGA GCGAAATTAA AAAGAAGTAT TTGTATGACT TAAAAGTTAA  
541 TGTTTTATCG GAAGCTGAGT TGACGTCAA AACAAAAGAA ACAAAGAAA AGTTAACCGC  
601 AACTTTTGAG CAGTTTAAAA AAGATACATT ACCAACAGAA CCAGAAAAAA AGGTAGCAGA  
661 AGCTCAGAAG AAGGTTGAAG AAGCTAAGAA AAAAGCCGAG GATCAAAAAG AAAAGATCG  
721 CCGTAACCTAC CCAACCATTA CTTACAAAAC GCTTGAACCT GAAATTGCTG AGTCCGATGT  
781 GGAAGTTAAA AAAGCGGAGC TTGAACTAGT AAAAGTGAAA GCTAAGGAAT CTCAAGACGA  
841 GGAAAAAATT AAGCAAGCAG AAGCGGAAGT TGAGAGTAAA CAAGCTGAGG CTACAAGGTT  
901 AAAAAAATC AAGACAGATC GTGAAGAAGC TAAACGAAAA GCAGATGCTA AGTTGAAGGA  
961 AGCTGTTGAA AAGAATGTAG CGACTTCAGA GCAAGATAAA CCAAAGAGGC

GGGCAAAACG

1021 AGGAGTTTCT GGAGAGCTAG CAACACCTGA TAAAAAGAA AATGATGCGA AGTCTTCAGA  
1081 TTCTAGCGTA GGTGAAGAAA CTCTTCCAAG CCCATCCCTT AATATGGCAA ATGAAAGTCA  
1141 GACAGAACAT AGGAAAGATG TCGATGAATA TATAAAAAA ATGTTGAGTG AGATCCAATT  
1201 AGATGGAAGA AACATACCC CAAATGTCAA CTTAAACATA AAGTTGAGCG CAATTTAAAC  
1261 GAAGTATTTG TATGAATTAA GTGTTTAAAG AGAGAACTCG AAAAAAGAAG AGTTGACGTC  
1321 AAAAACCAAA GCAGAGTTAA CCGCAGCTTT TGAGCAGTTT AAAAAAGATA CATTGAAACC  
1381 AGAAAAAATA GTAGCAGAAG CTGAGAAGAA GGTTGAAGAA GCTAAGAAAA

AAGCCAAGGA

1441 TCAAAAAGAA GAAGATCGCC GTAACCTACC AACCAATACT TACAAAACGC TTGAACTTGA  
1501 AATTGCTGAG TCCGATGTGA AAGTTAAAGA AGCGGAGCTT GAACTAGTAA

AAGAGGAAGC

1561 TAACGAATCT CGAAACGAGG AAAAAATTAA GCAAGCAAAA GAGAAAGTTG AGAGTAAAAA  
1621 AGCTGAGGCT ACAAGGTTAG AAAAAATCAA GACAGATCGT AAAAAAGCAG AAGAAGAAGC  
1681 TAAACGAAAA GCAGAAGAAT CTGAGAAAAA AGCTGCTGAA GCCAAACAAA AAGTGGATGC  
1741 TGAAGAATAT GCTCTTGAAG CTAAAATCGC TGAGTTGGAA TATGAAGTTC AGAGACTAGA  
1801 AAAAGAGCTC AAAGAGATTG ATGAGTCTGA CTCAGAAGAT TATCTTAAAG AAGGCCTCCG  
1861 TGCTCCTCTT CAATCTAAAT TGGATACCAA AAAAGCTAAA CTATCAAAAC TTGAAGAGTT  
1921 GAGTGATAAG ATTGATGAGT TAGACGCTGA AATTGCAAAA CTTGAAGTTC AACTTAAAGA  
1981 TGCTGAAGGA AACAATAATG TAGAAGCCTA CTTTAAAGAA GGTTTAGAGA AACTACTGCT  
2041 TGAGAAAAAA GCTGAATTAG AAAAGCTGA AGCTGACCTT AAGAAAGCAG TTGATGAGCC  
2101 AGAAACTCCA GCTCCGGCTC CTCAACCAGC TCCGGCTCCA GAAAAACCAG

CTGAAAAACC

2161 AGCTCCAGCT CCAGCTCCAG AAAAACCAGC TCCAGCTCCA GAAAAACCAG

CTCCAGCTCC

2221 AGAAAAACCA GCTCCAGCTC CAGAAAAACC AGCTCCAGCT CCAGAAAAAC

CAGCTCCAGC

2281 TCCAGAAAAA CCAGCTCCAG CTCCAGAAAA ACCAGCTCCA GCTCCTAAAC CAGAAACTCC

//

Fig. 18 (cont'd)

[illegible]

LOCUS BG8090.DNA 1680 BP SS-DNA

SYN

Fig. 19

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES Location/Qualifiers

CDS 220..1680

BASE COUNT 714 A 287 C 375 G 304 T 0 OTHER

ORIGIN -

1 ATTGTATACG ACTCACTATA GGGCGAATTG GGCCCGACGT CGCATGCTCC CGGCCGCCAT  
61 GGCCGCGGGA TTCGACGAAT AGCTGAAGAG GAAAAGCTAT TACATGAAGT TATAATCCCA  
121 AATGGAAGCA TAAAGAGATA AATACAAAAT TCGATTATA TACAGTTCAT ATTGAAGTGA  
181 TATAGTAAGG TTAAAGAAAA AATATAGAAG GAAATAAACA TGTTCATC AAAAACGAA  
241 AGAAAAGTAC ATTATTCAAT TCGTAAATTT AGTATTGGAG TAGCTAGTGT AGCTGTTGCC  
301 AGTCTTTTTA TGGGAAGTGT GGTTCATGCG ACAGAGAAGG AGGTAAGTAC CCAAGTAGCC  
361 ACTTCTTTTA ATAAGGCAAA TAAAGTCAG ACAGAACATA TGAAAGCTGC TAAACAAGTC  
421 GATGAATATA TAACAAAAAA GCTCCAATTA GATAGAAGAA AACATACCCA AAATGTCGGC  
481 TTAATCACAA AGTTGGGCGT AATTAAAACG GAGTATTTGC ATAGATTAAG TGTTTCAAAA  
541 GAGAAGTCGG AAGCTGAGTT GCCGTCAGAA ATAAAAGCAA AGTTAGACGC AGCTTTTGAG  
601 CAGTTTAAAA AAGATACATT ACCAACAGAA CCAGGAAAAA AGGTAGCAGA AGCTGAGAA  
661 AAGGTTGAAG AAGCTAAGAA AAAAGCCGAG GATCAAAAAG AAGAAGATCG TCGTAAGTAC  
721 CCAACCATTA CTTACAAAAC GCTTGAAGTT GAAATTGCTG AGTCCGATGT GGAAGTTAAA  
781 AAAGCGGAGC TTGAAGTAGT AAAAGAGGAA GCTAAGGGAT CTCGAAACGA GCAAAAAGTT  
841 AACCAAGCAA AAGCGAAAAG TGAGAGTAAA CAAGCTGAGG CTACAAGTT AAAAAAATC  
901 AAGACAGATC GTGAACAAGC TGAGACTACA AGGTTAGAAA ACATCAAGAC AGATCGTGAA  
961 AAAGCAGAAG AAGCTAAACG AAAAGCAGAT GCTAAAGAGC AAGATGAATC  
AAAGAGGCGG  
1021 GTAAAAGGAG GAGTTCCGGG AGAGCAAGCA AACTTGATA AAAAAGAAAA  
TGATGCGAAG  
1081 TCTTCAGATT CTAGCGTAGG TGAAGAACT CTTCCAAGCC CATCCCTGAA ATCAGGAAAA  
1141 AAGGTAGCAG AAGCTGAGAA GAAGGTTGCA GAAGCTGAGA AAAAAGCCAA  
GGATCAAAAA  
1201 GAAGAAGATC GCCGTAAC TAACCAACCAAT ACTTACAAAA CGCTTGAAGT TGAAATTGCT  
1261 GAGTCCGATG TGAAAGTTAA AGAAGCGGAG CTTGAACTAG TAAAGAGGAA  
AGCTAAGGAA  
1321 TCTCGAAACG AGGAAAAAGT TAAGCAAGCA AAAGCGGAAG TTGAGAGTAA  
AAAAGCTGAG  
1381 GCTACAAGGT TAGAAAAAAT CAAGACAGAT CGTAAAAAAG CAGAAGAAGC TAAACGAAAA  
1441 GCAGCAGAAG AAGATAAAGT TAAAGAAAAA CCAGCTGAAC AACCACAACC  
AGCGCCGGCT  
1501 CCTCAACCAG AAAAACCAGC TCCAGCTCCA AAACCAGAGA ATCCAGCTGA ACAACCAAAA  
1561 GCAGAAAAAC CAGCTGATCA ACAAGCTGAA GAAGACTATG CTCGTAGATC AGAAGAAGAA  
1621 TATAATCGCT TGAATCAACA GCAACCGCCA AAAACTGAAA AACCAGCACA ACCATCTACT

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LOCUS L81905.DNA 1766 BP SS-DNA

SYN

Fig. 20

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES Location/Qualifiers

CDS 217..1766

BASE COUNT 741 A 313 C 402 G 309 T 1 OTHER

ORIGIN -

1 GTATACGACT CACTATAGGG CGAATTGGGC CCGACGTCGC ATGCTCCCGG

CCGCCATGGC

61 CGCGGGATTG GACGAATAGC TGAAGAGGAA AAGCTATTAC ATGAAGTTAT AATCCCAAAT

121 GGAAGCATAA AGAGATAAAT ACAAATTCG ATTTATATAC AGTTCATATT GAAGTGATAT

181 AGTAAGGTTA AAGAAAAAAT ATAGAAGGAA ATAAACATGT TTGCATCAA AAGCGAAAGA

241 AAAGTACATT ATTCAATTCG TAAATTTAGT GTTGGAGTAG CTAGTGTAGT TGTGCCAGT

301 CTTGTTATGG GAAGTGTGGT TCATGCGACA GAGAACGAGG GAGCTACCCA

AGTACCCACT

361 TCTTCTAATA GGGCAAATGA AAGTCAGGCA GAACAAGGAG AACAACCTAA AAAACTCGAT

421 TCAGAACGAG ATAAGGCAAG GAAAGAGGTC GAGGAATATG TAAAAAAAT AGTGGGTGAG

481 AGCTATGCAA AATCAACTAA AAAGCGACAT ACAATTACTG TAGCTCTAGT TAACGAGTTG

541 AACAACATTA AGAACGAGTA TTTGAATAAA ATAGTTGAAT CAACCTCAGA AAGCCAACTA

601 CAGATACTGA TGATGGAGAG TCGATCAAAA GTAGATGAAG CTGTGTCTAA GTTTGAAAAG

661 GACTCATCTT CTTGTCAGG TTCAGACTCT TCCACTAAAC CGGAAGCTTC AGATACAGCG

721 AAGCCAAACA AGCCGACAGA ACCAGGAGAA AAGGTAGCAG AAGCTAAGAA

GAAGGTTGAA

781 GAAGCTGAGA AAAAAGCCAA GGATCAAAAA GAAGAAGATC GTCGTAACCTA CCCAACCATT

841 ACTTACAAAA CGCTTGAAGT TGAAATTGCT GAGTCCGATG TGGAAGTTAA AAAAGCGGAG

901 CTTGAAGTAG TAAAAGTGAA AGCTAACGAA CCTCGAGACG AGCAAAAAAT TAAGCAAGCA

961 GAAGCGGAAG TTGAGAGTAA ACAAGCTGAG GCTACAAGGT TAAAAAAAT CAAGACAGAT

1021 CGTGAAGAAG CAGAAGAAGA AGCTAAACGA AGAGCAGATG CTAAAGAGCA

AGGTAAACCA

1081 AAGGGGCGGG CAAAACGAGG AGTTCCTGGA GAGCTAGCAA CACCTGATAA

AAAAGAAAAT

1141 GATGCGAAGT CTTAGATTG TAGCGTAGGT GAAGAACTC TTCCAAGCCC ATCCCTGAAA

1201 CCAGAAAAAA AGGTAGCAGA AGCTGAGAAG AAGGTTGAAG AAGCTAAGAA

AAAAGCCGAG

1261 GATCAAAAAG AAGAAGATCG CCGTAACCTAC CCAACCAATA CTTACAAAAC GCTTGAAGTT

1321 GAAATTGCTG AGTCCGATGT GGAAGTTAAA AAAGCGGAGC TTGAACTAGT AAAAGAGGAA

1381 GCTAAGGAAC CTCGAAACGA GGAAAAAGTT AAGCAAGCAA AAGCGGAAGT

TGAGAGTAAA

1441 AAAGCTGAGG CTACTAGGTT AGAAAAATC AAGACAGATC GTAAAAAAGC AGAAGAAGAA

1501 GCTAAACGAA AAGCAGCAGA AGAAGATAAA GTTAAAGAAA AACCAGCTGA ACAACCACAA

1561 CCAGCGCCGG CTCCAAAAGC AGAAAAACCA GCTCCAGCTC CAAAACCAGA

GAATCCAGCT

1621 GAACAACCAA AAGCAGAAAA ACCAGCTGAT CAACAAGCTG AAGAAGAGTA TGCTCGTAGA

1681 TCAGAAGAAG AATATAATCG CTTGACTCTA CAGCAACCGC CAAAACTGA AAAACCAGCA

1741 CAACCATCTA CTCCAAAAC AAANAC

//


LOCUS DBL6A.DNA 1590 BP SS-DNA SYN   
DEFINITION -  
ACCESSION -  
KEYWORDS -  
SOURCE -  
FEATURES Location/Qualifiers  
CDS 127..1590  
BASE COUNT 701 A 261 C 339 G 288 T 1 OTHER  
ORIGIN -

Fig. 21

1 AAACATTAC ATGAAGTTAT AATCCCAAAT GGAAGCATAA AGAGATAAAT ACAAAATTCTG  
61 ATTTATATAC AGTTCATATT GAAGTGATAT AGTAAGGTTA AAGAAAAAAT ATAGAAGGAA  
121 ATAATTATGT TTGCATCYAA AAGCGAAAGA AAAGTACATT ATTCAATTCTG TAAATTTAGT  
181 ATTGGAGTAG CTAGTGTAGC TGTTGCTAGC TTGTTCTTAG GAGGAGTAGT CCATGCAGAA  
241 GGGGTTAGAA GTGAGAATAC CCCCAAGGTT ACATCTAGTG GGGATGAAGT CGATGAATAT  
301 ATAAAAAATA TGTTGAGTGA GATCCAATTA GATAAAAGAA AACATACCCA CAATTTCTGCC  
361 TTAAACCTAA AGTTGAGCAG AATTAACACG GAGTATTTGT ATAAATTAAA AGTTAATGTT  
421 TTAGAAGAAA AGTCAAAAGC TGAGTTGACG TCAAAAACAA AAAAAGAGGT AGACGCAGCT  
481 TTTGAGAAGT TTAAGAAAGA TACATTGAAA CTAGGAGAAA AGGTAGCAGA AGCTCAGAAG  
541 AAGGTTGAAG AAGCTAAGAA AAAAGCCAAG GATCAAAAAG AAGAAGATCA CCGTAAGTAC  
601 CCAACCAATA CTTACAAAAC GCTTGAACCT GAAATTGCTG AGTCCGATGT GAAAGTTAAA  
661 GAAGCGGAGC TTGAACTATT GAAAGAGGAA GCTAAACTC GAAACGAGGA CACAATTAAC  
721 CAAGCAAAAG CGAAAGTTAA GAGTGAACAA GCTGAGGCTA CAAGGTTAAA AAAAATCAAG  
781 ACAGATCGTG AACAAGCTGA GGCTACAAGG TTAGAAAACA TCAAGACAGA TCGTGAAAAA  
841 GCAGAAGAAG CTAAACGAAA AGCAGAAGCA GAAGAAGTTA AAGATAAACT AAAGAGGCGG  
901 ACAAACGAG CAGTTCCTGG AGAGCCAGCA ACACCTGATA AAAAAGAAAA TGATGCGAAG  
961 TCTTCAGATT CTAGCGTAGG TGAAGAACT CTTCCAAGCC CATCCCTGAA ATCAGGAAAA  
1021 AAGGTAGCAG AAGCTCAGAA GAAGGTAGCA GAAGCTGAGA AAAAAGCCAA  
GGATCAAAAA  
1081 GAAGAAGATC GCCGTAACCTA CCCAACCAAT ACTTACAAAA CGCTTGACCT TGAAATTGCT  
1141 GAGTCCGATG TGAAAGTTAA AGAAGCGGAG CTTGAACTAG TAAAGAGGA  
AGCTAAGGAA  
1201 TCTCGAAACG AGGAAAAAGT TAAGCAAGCA AAAGCGAAAG TTGAGAGTAA AAAAGCTGAG  
1261 GCTACAAGGT TAGAAAAAAT CAAGACAGAT CGTAAAAAG CAGAAGAAGC TAAACGAAGA  
1321 GCAGCAGAAG AAGATAAAGT TAAAGAAAAA CCAGCTGAAC AACCACAACC  
AGCGCCGGCT  
1381 CCTCAACCAG AAAAACCAAC TGAAGAGCCT GAGAATCCAG CTCCAGCTCC  
AAAACCTGAG  
1441 AATCCAGCTG AACAACCAAA AGCAGAAAAA CCAGCTGATC AACAAGCTGA AGAAGACTAT  
1501 GCTCGTAGAT CAGAAGAAGA ATATAATCGC TTGACTCAAC AGCAACCGCC AAAAAGTGA  
1561 AAACCAGCAC AACCATCTAC TCCAAAAACA

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